

LISTE DE SÉQUENCES.

NOMBRE DE SÉQUENCES : 6

5 INFORMATION CONCERNANT LA SEQ ID NO:1 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR : 3562 paires de base

B) TYPE : acide nucléique

10 C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : rat

15

ix) CARACTERISTIQUE

A) NOM/CLE : ASIC

B) LOCALISATION : 123 .. 1700

20 xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:1 :

CACACACACA CACACACACA CACACACACA CACACACACA CACACAGAAC CTGCGCCTGT 60

GCCTGTGCCT GTGCCTGTGC CTGTTTGAGA GCTGGAGACA CAGAAGGATC CCCTTGGCAA 120

25 GG ATG GAA TTG AAG ACC GAG GAG GAG GAG GTG GGT GGT GTC CAG CCG 167
 Met Glu Leu Lys Thr Glu Glu Glu Glu Val Gly Gly Val Gln Pro
 1 5 10 15

30 GTG AGC ATC CAG GCT TTC GCC AGC AGC TCC ACG CTG CAT GGT CTT GCC 215
 Val Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Leu Ala
 20 25 30

35 CAC ATC TTC TCC TAT GAG CGG CTG TCT CTG AAG CGG GCA CTG TGG GCC 263
 His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp Ala
 35 40 45

40 CTG TGC TTC CTG GGT TCG CTG GCC GTC CTG CTG TGT GTG TGC ACT GAG 311
 Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr Glu
 50 55 60

45 CGT GTG CAG TAC TAC TTC TGC TAT CAC CAC GTC ACC AAG CTT GAC GAA 359
 Arg Val Gln Tyr Tyr Phe Cys Tyr His His Val Thr Lys Leu Asp Glu
 65 70 75

50 GTG GCT GCC TCC CAG CTC ACC TTC CCT GCT GTC ACA CTG TGC AAT CTC 407
 Val Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Leu
 80 85 90 95

55 AAT GAG TTC CGC TTT AGC CAA GTC TCC AAG AAT GAC CTG TAC CAT GCT 455
 Asn Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His Ala
 100 105 110

55 GGG GAG CTG CTG GCC CTG CTC AAC AAC AGG TAT GAG ATC CCG GAC ACA 503
 Gly Glu Leu Leu Ala Leu Leu Asn Arg Tyr Glu Ile Pro Asp Thr
 115 120 125

	CAG Gln	ATG Met	GCT Ala	GAT Asp	GAA Glu	AAG Lys	CAG Gln	CTA Leu	GAG Glu	ATA Ile	TTG Leu	CAG Gln	GAC Asp	AAG Lys	GCC Ala	AAC Asn	551
			130					135					140				
5	TTC Phe	CGG Arg	AGC Ser	TTC Phe	AAG Lys	CCC Pro	AAG Lys	CCC Pro	TTC Phe	AAC Asn	ATG Met	CGT Arg	GAA Glu	TTC Phe	TAC Tyr	GAC Asp	599
		145					150					155					
10	AGA Arg	GCG Ala	GGG Gly	CAC His	GAT Asp	ATT Ile	CGA Arg	GAC Asp	ATG Met	CTG Leu	CTC Leu	TCG Ser	TGC Cys	CAC His	TTC Phe	CGT Arg	647
	160					165					170					175	
15	GGG Gly	GAG Glu	GCC Ala	TGC Cys	AGC Ser	GCT Ala	GAA Glu	GAT Asp	TTC Phe	AAA Lys	GTG Val	GTC Val	TTC Phe	ACT Thr	CGG Arg	TAT Tyr	695
					180					185					190		
20	GGG Gly	AAG Lys	TGT Cys	TAC Tyr	ACA Thr	TTC Phe	AAC Asn	TCG Ser	GGC Gly	CAA Gln	GAT Asp	GGG Gly	CGG Arg	CCA Pro	CGG Arg	CTG Leu	743
				195					200					205			
25	AAG Lys	ACC Thr	ATG Met	AAA Lys	GGT Gly	GGG Gly	ACT Thr	GGC Gly	AAT Asn	GGC Gly	CTG Leu	GAG Glu	ATC Ile	ATG Met	CTG Leu	GAC Asp	791
			210					215					220				
30	ATT Ile	CAG Gln	CAA Gln	GAT Asp	GAA Glu	TAT Tyr	TTG Leu	CCT Pro	GTG Val	TGG Trp	GGA Gly	GAG Glu	ACC Thr	GAC Asp	GAG Glu	ACA Thr	839
		225					230					235					
35	TCC Ser	TTC Phe	GAA Glu	GCA Ala	GGC Gly	ATC Ile	AAA Lys	GTG Val	CAG Gln	ATC Ile	CAC His	AGT Ser	CAG Gln	GAT Asp	GAA Glu	CCC Pro	887
	240					245					250					255	
40	CCT Pro	TTC Phe	ATC Ile	GAC Asp	CAG Gln	CTG Leu	GGC Gly	TTT Phe	GGT Gly	GTG Val	GCT Ala	CCA Pro	GGT Gly	TTC Phe	CAG Gln	ACG Thr	935
					260					265					270		
45	TTT Phe	GTG Val	TCT Ser	TGC Cys	CAG Gln	GAG Glu	CAG Gln	AGG Arg	CTC Leu	ATC Ile	TAC Tyr	CTG Leu	CCC Pro	TCA Ser	CCC Pro	TGG Trp	983
				275					280					285			
50	GGC Gly	ACC Thr	TGC Cys	AAT Asn	GCT Ala	GTT Val	ACC Thr	ATG Met	GAC Asp	TCG Ser	GAT Asp	TTC Phe	TTC Phe	GAC Asp	TCC Ser	TAC Tyr	1031
			290					295					300				
55	AGC Ser	ATC Ile	ACT Thr	GCC Ala	TGC Cys	CGG Arg	ATT Ile	GAT Asp	TGC Cys	GAG Glu	ACG Thr	CGT Arg	TAC Tyr	CTG Leu	GTG Val	GAG Glu	1079
		305					310					315					
60	AAC Asn	TGC Cys	AAC Asn	TGC Cys	CGT Arg	ATG Met	GTG Val	CAC His	ATG Met	CCA Pro	GGG Gly	GAC Asp	GCC Ala	CCA Pro	TAC Tyr	TGC Cys	1127
	320					325					330					335	
65	ACT Thr	CCA Pro	GAG Glu	CAG Gln	TAC Tyr	AAG Lys	GAG Glu	TGT Cys	GCA Ala	GAT Asp	CCT Pro	GCC Ala	CTG Leu	GAC Asp	TTC Phe	CTA Leu	1175
					340					345					350		
70	GTG Val	GAG Glu	AAA Lys	GAC Asp	CAG Gln	GAA Glu	TAC Tyr	TGC Cys	GTG Val	TGT Cys	GAG Glu	ATG Met	CCT Pro	TGC Cys	AAC Asn	CTG Leu	1223
				355					360					365			

	ACC CGC TAC GGC AAG GAG CTG TCC ATG GTC AAG ATC CCA AGC AAA GCC	1271
	Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala	
	370 375 380	
5	TCC GCC AAG TAC CTG GCC AAG AAG TTC AAC AAA TCG GAG CAG TAC ATA	1319
	Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile	
	385 390 395	
10	GGG GAG AAC ATT CTG GTG CTG GAC ATT TTC TTT GAA GTC CTC AAC TAT	1367
	Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr	
	400 405 410 415	
15	GAG ACC ATC GAG CAG AAA AAG GCC TAT GAG ATC GCA GGG CTG TTG GGT	1415
	Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly	
	420 425 430	
20	GAC ATC GGG GGC CAG ATG GGG TTG TTC ATC GGT GCC AGC ATC CTC ACC	1463
	Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr	
	435 440 445	
25	GTG CTG GAA CTC TTT GAC TAT GCC TAC GAG GTC ATT AAG CAC AGG CTG	1511
	Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu	
	450 455 460	
30	TGC AGA CGT GGA AAG TGC CAG AAG GAG GCT AAG AGG AGC AGC GCA GAC	1559
	Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp	
	465 470 475	
35	AAG GGC GTG GCG CTC AGC CTG GAT GAC GTC AAA AGA CAC AAT CCC TGC	1607
	Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys	
	480 485 490 495	
40	GAG AGC CTC CGA GGA CAT CCT GCC GGG ATG ACG TAC GCT GCC AAC ATC	1655
	Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile	
	500 505 510	
45	CTA CCT CAC CAT CCC GCT CGA GGC ACG TTT GAG GAC TTT ACC TGC TAA	1703
	Leu Pro His His Pro Ala Arg Gly Thr Phe Glu Asp Phe Thr Cys *	
	515 520 526	
50	GCCCTCGCAG GCCGCTGTAC CAAAGGCCTA GGTGGGGAGG GCTGGGGGAG CAAGGGGCCC	1763
	CCAAGTGGCC CCAGCTACCC TGTGGACTTA ACTGCATTCC TGGTCAGTGG TTCCCTCTTG	1823
	TCTGTGGTGA GAAAGGAGTC TTGACCATAG AGTCCTCTCC CAGCCTCTAT CCCATCTTTT	1943
	TATTTTAATT TAATCACATT TGCTCTGTAA TATTGCTTGA GGCTGGGGAT CGTGATTTCC	2003
	CCCCAGTTCT TTTATTGTTG AGAATAGTTT TCTCTATTCT GGGTTTCTG TTATTTCAAA	2063
	TGAATCTGCA AATTGCTCTT CCCATCTCTA TGAAGAATTG CGTTGGAATT TTGATGGGGA	2123
	TTGTATTGAA TCTGTAGATT GCCTTTGGTA AGATGGCCAT TTTTACTATG TTAATCCTGC	2183
	CAATTCATGA GCAAGGGAGA TCTTTCTATC TCTGAAATCT ACTTCAGTTT CTTTCTTCAG	2243
55	AGACTTGAAG TTCTTGTCAT AAAAATCTTT TTGGTTAGAG CCACACCAAG GTATTTTATA	2303
	TTGTTTGTGA CTATTGTGAA TGGTGTCAAT TCCCTAATTT CCTTCTCAGC CTACTTATCC	2363

	TTTGAGTAGA	GGAAGGCTTC	TGATTTGTTT	GGGTAAATTT	TATACCCAGC	TGCTTTGCTA	2423
	AAGTTCTTTA	TCAGGTTTAG	GTGTTCTCTG	GTGGAACTTT	TGGGGTCACG	TAAGAATACT	2483
5	ATTATATCAT	CTGCAAATAG	TGATATTTCA	CTTCTTCCTT	TCCAATTTCT	ATCCCTCTGG	2543
	GGACTTTTTG	TTGTCTAATT	GCTCTGGCTA	GGACTTCAAA	TTCTATATTG	AATAGATAGG	2603
	GAGAGAGTGG	GCAGCCTTGT	CTAGTTCCTG	GTTTTCTGTG	GATCGCTTCA	AATTTCTCTC	2663
10	CATTTAGTTT	GATATTGGCT	ACTGGTTTGC	TGTATATGGC	TTTTACTGTA	CTTAGGTATG	2723
	GGCCTTGAAT	TCCTGATATT	TCCAAGACTT	TTAACATGAA	GGGGTTTTGA	AATTTGCCAA	2783
15	ATGCTTTCTC	AGCATCTAAT	GAGATGATCA	TGTGCCCTCC	CCCCACCTTG	AGTTTGTTTA	2843
	TATAGTGGGT	TACATGAAAG	GATCATTTCT	AATAGTCCAC	AAGTCTGCCA	AATCTTGCTG	2903
	ATTGTGACTC	ATTTCCATAG	CAGGCTCTAT	AACTTCTCTA	ACAGATTGCA	TTAAACTCTG	2963
20	CTTGGGGAAG	GCATTACCTC	TTGGTTGAAG	CAATGTTGTA	GTTTCTATGC	CTGCTGAGTA	3023
	AATAGCCTCA	AGTCCAAGTA	CTTGCCCAGA	CTAATGATCA	AACGTATCCA	GGAGTTCCAT	3083
25	ACCAGAGATG	TACTCTTCTC	TCCTTTGAAG	TACATTGCTG	GAAGAGTAAT	TGTGTTTGCT	3143
	AGAGATACTC	CTTCGAACTG	CAAAAGAAAT	CTCTTGCTA	AGCATATAAT	CAAGCCTCAG	3203
	GTTTTCTTTT	TATTAAATAG	CTGCTTGTA	GAAAGTGGAC	ACTAAGCATA	TACCTCAAAG	3263
30	GGAGACAGAA	TGACTCTGTG	CCTTCACTGA	TGGAAGTCTG	GGTTACAAAT	TACATCAGAA	3323
	GAACCTATCA	TAGTGAAACA	TCTCATTTCC	CTGGTATAAT	CCCTTCTAGA	AATACACTTG	3383
35	TGACTCTGAA	ATGTTATAAT	CGTGACAACT	AGGCTGTTAC	AGATACACCA	AGTTAAATTT	3443
	GATAGAGAAA	CCAGGCTTGG	AGCCTCATGT	CCATAGGGCA	AGAGGAAGAT	GCTGAGTGTT	3503
	TAAGGTGGT	TTGAGCGAAG	AACAATACCT	TGTGTCACAA	AAATGAAAGG	AAAAAAGAAA	3563
40	AAAGGAAAGA	AGGAAAGAAA	GAGAGAGAAA	GAAAAAGAAA	GAAAGAAAAA	AAAAAAAAA	3562

INFORMATION CONCERNANT LA SEQ ID NO:2 :

i) CARACTERISTIQUE DE LA SEQUENCE :
 A) LONGUEUR : 1620 paires de base
 5 B) TYPE : acide nucléique
 C) NOMBRE DE BRINS : double
 D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN
 10 vi) ORIGINE : homme

ix) CARACTERISTIQUE
 A) NOM/CLE : ASIC
 B) LOCALISATION : 1 .. 1542
 15

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:2 :

20	CCG GTG AGC ATC CAG GCC TTC GCC AGC AGC TCC ACA CTG CAC GGC ATG	48
	Pro Val Ser Ile Gln Ala Phe Ala Ser Ser Ser Thr Leu His Gly Met	
	1 5 10 15	
25	GCC CAC ATC TTC TCC TAC GAG CGG CTG TCT CTG AAG CGG GCA CTG TGG	96
	Ala His Ile Phe Ser Tyr Glu Arg Leu Ser Leu Lys Arg Ala Leu Trp	
	20 25 30	
30	GCC CTG TGC TTC CTG GGC TCG CTG GCT GTG CTG CTG TGT GTG TGC ACG	144
	Ala Leu Cys Phe Leu Gly Ser Leu Ala Val Leu Leu Cys Val Cys Thr	
	35 40 45	
35	GAG CGT GTG CAG TAC TAC TTC CAC TAC CAC CAT GTC ACC AAG CTC GAC	192
	Glu Arg Val Gln Tyr Tyr Phe His Tyr His His Val Thr Lys Leu Asp	
	50 55 60	
40	GAG GTG GCT GCC TCT CAG CTT ACC TTC CCT GCT GTC ACG CTG TGC AAC	240
	Glu Val Ala Ala Ser Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn	
	65 70 75 80	
45	CTC AAC GAG TTC CGC TTT AGC CAA GTC TCC AAG AAT GAC CTG TAT CAT	288
	Leu Asn Glu Phe Arg Phe Ser Gln Val Ser Lys Asn Asp Leu Tyr His	
	85 90 95	
50	GCT GGG GAG CTG CTG GCC CTG CTC AAC AAC AGG TAT GAG ATA CCA GAC	336
	Ala Gly Glu Leu Leu Ala Leu Leu Asn Asn Arg Tyr Glu Ile Pro Asp	
	100 105 110	
55	ACA CAG ATG GCA GAT GAA AAG CAG CTG GAG ATA CTG CAG GAC AAA GCC	384
	Thr Gln Met Ala Asp Glu Lys Gln Leu Glu Ile Leu Gln Asp Lys Ala	
	115 120 125	
50	AAC TTC CGC AGC TTC AAA CCC AAA CCC TTC AAC ATG CGT GAG TTC TAC	432
	Asn Phe Arg Ser Phe Lys Pro Lys Pro Phe Asn Met Arg Glu Phe Tyr	
	130 135 140	
55	GAC CGA GCT GGG CAC GAC ATT CGA GAC ATG CTG CTC TCC TGC CAC TTC	480
	Asp Arg Ala Gly His Asp Ile Arg Asp Met Leu Leu Ser Cys His Phe	
	145 150 155 160	

		CGG	GGG	GAG	GTC	TGC	AGC	GCT	GAA	GAC	TTC	AAG	GTG	GTC	TTC	ACA	CGC	528
		Arg	Gly	Glu	Val	Cys	Ser	Ala	Glu	Asp	Phe	Lys	Val	Val	Phe	Thr	Arg	
					165						170					175		
5		TAT	GGA	AAG	TGC	TAC	ACG	TTC	AAC	TCG	GGC	CGA	AAT	GGG	CGG	CCG	CGG	576
		Tyr	Gly	Lys	Cys	Tyr	Thr	Phe	Asn	Ser	Gly	Arg	Asn	Gly	Arg	Pro	Arg	
					180					185					190			
10		CTG	AAG	ACC	ATG	AAG	GGT	GGG	ACG	GGC	AAT	GGG	CTG	GAA	ATC	ATG	CTG	624
		Leu	Lys	Thr	Met	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	Glu	Ile	Met	Leu	
				195					200					205				
15		GAC	ATC	CAG	CAG	GAC	GAG	TAC	CTG	CCT	GTG	TGG	GGG	GAG	ACT	GAC	GAG	672
		Asp	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Val	Trp	Gly	Glu	Thr	Asp	Glu	
			210					215					220					
20		ACG	TCT	TTC	GAA	GCA	GGC	ATC	AAA	GTG	CAG	ATC	CAT	AGT	CAG	GAT	GAA	720
		Thr	Ser	Phe	Glu	Ala	Gly	Ile	Lys	Val	Gln	Ile	His	Ser	Gln	Asp	Glu	
			225				230					235					240	
25		CCT	CCT	TTC	ATC	GAC	CAG	CTG	GGC	TTT	GGC	GTG	GCC	CCA	GGC	TTC	CAG	768
		Pro	Pro	Phe	Ile	Asp	Gln	Leu	Gly	Phe	Gly	Val	Ala	Pro	Gly	Phe	Gln	
					245						250					255		
30		ACC	TTT	GTG	GCC	TGC	CAG	GAG	CAG	CGG	CTC	ATA	TAC	CTG	CCC	CCA	CCC	816
		Thr	Phe	Val	Ala	Cys	Gln	Glu	Gln	Arg	Leu	Ile	Tyr	Leu	Pro	Pro	Pro	
					260					265					270			
35		TGG	GGC	ACC	TGC	AAA	GCT	GTT	ACC	ATG	GAC	TCG	GAT	TTG	GAT	TTC	TTC	864
		Trp	Gly	Thr	Cys	Lys	Ala	Val	Thr	Met	Asp	Ser	Asp	Leu	Asp	Phe	Phe	
				275				280						285				
40		GAC	TCC	TAC	AGC	ATC	ACT	GCC	TGC	CGC	ATC	GAC	TGT	GAG	ACG	CGC	TAC	912
		Asp	Ser	Tyr	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	Arg	Tyr	
			290					295					300					
45		CTG	GTG	GAG	AAC	TGC	AAC	TGC	CGC	ATG	GTG	CAC	ATG	CCA	GGG	GAT	GCC	960
		Leu	Val	Glu	Asn	Cys	Asn	Cys	Arg	Met	Val	His	Met	Pro	Gly	Asp	Ala	
			305			310						315					320	
50		CCA	TAC	TGT	ACT	CCA	GAG	CAG	TAC	AAG	GAG	TGT	GCA	GAT	CCT	GCT	CTG	1008
		Pro	Tyr	Cys	Thr	Pro	Glu	Gln	Tyr	Lys	Glu	Cys	Ala	Asp	Pro	Ala	Leu	
					325						330					335		
55		GAC	TTC	CTG	GTG	GAG	AAG	GAC	CAG	GAG	TAC	TGC	GTG	TGT	GAA	ATG	CCT	1056
		Asp	Phe	Leu	Val	Glu	Lys	Asp	Gln	Glu	Tyr	Cys	Val	Cys	Glu	Met	Pro	
					340				345					350				
60		TGC	AAC	CTG	ACC	CGC	TAT	GGC	AAA	GAG	CTG	TCC	ATG	GTC	AAG	ATC	CCC	1104
		Cys	Asn	Leu	Thr	Arg	Tyr	Gly	Lys	Glu	Leu	Ser	Met	Val	Lys	Ile	Pro	
				355				360						365				
65		AGC	AAA	GCC	TCA	GCC	AAG	TAC	CTG	GCC	AAG	AAG	TTC	AAC	AAA	TCT	GAG	1152
		Ser	Lys	Ala	Ser	Ala	Lys	Tyr	Leu	Ala	Lys	Lys	Phe	Asn	Lys	Ser	Glu	
			370					375					380					
70		CAA	TAC	ATA	GGG	GAG	AAC	ATC	CTG	GTG	CTG	GAC	ATT	TTC	TTT	GAA	GTC	1200
		Gln	Tyr	Ile	Gly	Glu	Asn	Ile	Leu	Val	Leu	Asp	Ile	Phe	Phe	Glu	Val	
						385		390				395					400	

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INFORMATION CONCERNANT LA SEQ ID NO:3 :

i) CARACTÉRISTIQUE DE LA SEQUENCE :
 A) LONGUEUR : 1666 paires de base
 5 B) TYPE : acide nucléique
 C) NOMBRE DE BRINS : double
 D) CONFIGURATION : linéaire

 ii) TYPE DE MOLECULE : ADN
 10 vi) ORIGINE : homme

 ix) CARACTÉRISTIQUE
 A) NOM/CLE : MDEG
 B) LOCALISATION : 127 .. 1663
 15 xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:3 :

	TCTGGCGCGA TGCTTACCTT GCGTTCTCTC CCCTGAACGT CAAGGTTTAA GCAGAGCCCCG	60
20	AGGACTGGGA GCTCTTCTCT GAAATTCGAT CAACCTGAAG CCAGTTGCGG AACTGCACGG	120
	GGTCCCCG ATG GAC CTC AAG GAA AGC CCC AGT GAG GGC AGC CTG CAA CCT	169
	Met Asp Leu Lys Glu Ser Pro Ser Glu Gly Ser Leu Gln Pro	
	1 5 10	
25	TCT AGC ATC CAG ATC TTT GCC AAC ACC TCC ACC CTC CAT GGC ATC CGC	217
	Ser Ser Ile Gln Ile Phe Ala Asn Thr Ser Thr Leu His Gly Ile Arg	
	15 20 25 30	
30	CAC ATC TTC GTG TAT GGG CCG CTG ACC ATC CGG CGT GTG CTG TGG GCA	265
	His Ile Phe Val Tyr Gly Pro Leu Thr Ile Arg Arg Val Leu Trp Ala	
	35 40 45	
35	GTG GCC TTC GTG GGC TCT CTG GGC CTG CTG CTG GTG GAG AGC TCT GAG	313
	Val Ala Phe Val Gly Ser Leu Gly Leu Leu Leu Val Glu Ser Ser Glu	
	50 55 60	
40	AGG GTG TCC TAC TAC TTC TCC TAC CAG CAT GTC ACT AAG GTG GAC GAA	361
	Arg Val Ser Tyr Tyr Phe Ser Tyr Gln His Val Thr Lys Val Asp Glu	
	65 70 75	
45	GTG GTG GCT CAA AGC CTG GTC TTC CCA GCT GTG ACC CTC TGT AAC CTC	409
	Val Val Ala Gln Ser Leu Val Phe Pro Ala Val Thr Leu Cys Asn Leu	
	80 85 90	
50	AAT GGC TTC CGG TTC TCC AGG CTC ACC ACC AAC GAC CTG TAC CAT GCT	457
	Asn Gly Phe Arg Phe Ser Arg Leu Thr Thr Asn Asp Leu Tyr His Ala	
	95 100 105 110	
55	GGG GAG CTG CTG GCC CTG CTG GAT GTC AAC CTG CAG ATC CCG GAC CCC	505
	Gly Glu Leu Leu Ala Leu Leu Asp Val Asn Leu Gln Ile Pro Asp Pro	
	115 120 125	
55	CAT CTG GCT GAC CCC TCC GTG CTG GAG GCC CTG CGG CAG AAG GCC AAC	553
	His Leu Ala Asp Pro Ser Val Leu Glu Ala Leu Arg Gln Lys Ala Asn	
	130 135 140	

	TTC	AAG	CAC	TAC	AAA	CCC	AAG	CAG	TTC	AGC	ATG	CTG	GAG	TTC	CTG	CAC	601
	Phe	Lys	His	Tyr	Lys	Pro	Lys	Gln	Phe	Ser	Met	Leu	Glu	Phe	Leu	His	
			145					150					155				
5	CGT	GTG	GGC	CAT	GAC	CTG	AAG	GAT	ATG	ATG	CTC	TAC	TGC	AAG	TTC	AAA	649
	Arg	Val	Gly	His	Asp	Leu	Lys	Asp	Met	Met	Leu	Tyr	Cys	Lys	Phe	Lys	
		160					165					170					
10	GGG	CAG	GAG	TGC	GGC	CAC	CAA	GAC	TTC	ACC	ACA	GTG	TTT	ACA	AAA	TAT	697
	Gly	Gln	Glu	Cys	Gly	His	Gln	Asp	Phe	Thr	Thr	Val	Phe	Thr	Lys	Tyr	
	175					180					185					190	
15	GGG	AAG	TGT	TAC	ATG	TTT	AAC	TCA	GGC	GAG	GAT	GGC	AAA	CCT	CTG	CTC	745
	Gly	Lys	Cys	Tyr	Met	Phe	Asn	Ser	Gly	Glu	Asp	Gly	Lys	Pro	Leu	Leu	
					195					200					205		
20	ACC	ACG	GTC	AAG	GGG	GGG	ACA	GGC	AAC	GGG	CTG	GAG	ATC	ATG	CTG	GAC	793
	Thr	Thr	Val	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	Glu	Ile	Met	Leu	Asp	
				210				215						220			
25	ATT	CAG	CAG	GAT	GAG	TAC	CTG	CCC	ATC	TGG	GGA	GAG	ACA	GAG	GAA	ACG	841
	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Ile	Trp	Gly	Glu	Thr	Glu	Glu	Thr	
			225					230					235				
30	ACA	TTT	GAA	GCA	GGA	GTG	AAA	GTT	CAG	ATC	CAC	AGT	CAG	TCT	GAG	CCA	889
	Thr	Phe	Glu	Ala	Gly	Val	Lys	Val	Gln	Ile	His	Ser	Gln	Ser	Glu	Pro	
		240					245					250					
35	CCT	TTC	ATC	CAA	GAG	CTG	GGC	TTT	GGG	GTG	GCT	CCA	GGG	TTC	CAG	ACC	937
	Pro	Phe	Ile	Gln	Glu	Leu	Gly	Phe	Gly	Val	Ala	Pro	Gly	Phe	Gln	Thr	
	255					260					265					270	
40	TTT	GTG	GCC	ACA	CAG	GAG	CAG	AGG	CTC	ACA	TAC	CTG	CCC	CCA	CCG	TGG	985
	Phe	Val	Ala	Thr	Gln	Glu	Gln	Arg	Leu	Thr	Tyr	Leu	Pro	Pro	Pro	Trp	
				275						280					285		
45	GGT	GAG	TGC	CGA	TCC	TCA	GAG	ATG	GGC	CTC	GAC	TTT	TTT	CCT	GTT	TAC	1033
	Gly	Glu	Cys	Arg	Ser	Ser	Glu	Met	Gly	Leu	Asp	Phe	Phe	Pro	Val	Tyr	
				290					295					300			
50	AGC	ATC	ACC	GCC	TGT	AGG	ATT	GAC	TGT	GAG	ACC	CGC	TAC	ATT	GTG	GAA	1081
	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	Arg	Tyr	Ile	Val	Glu	
			305					310					315				
55	AAC	TGC	AAC	TGC	CGC	ATG	GTT	CAC	ATG	CCA	GGG	GAT	GCC	CCT	TTT	TGT	1129
	Asn	Cys	Asn	Cys	Arg	Met	Val	His	Met	Pro	Gly	Asp	Ala	Pro	Phe	Cys	
		320					325					330					
60	ACC	CCT	GAG	CAG	CAC	AAG	GAG	TGT	GCA	GAG	CCT	GCC	CTA	GGT	CTG	TTG	1177
	Thr	Pro	Glu	Gln	His	Lys	Glu	Cys	Ala	Glu	Pro	Ala	Leu	Gly	Leu	Leu	
	335					340					345					350	
65	GCG	GAA	AAG	GAC	AGC	AAT	TAC	TGT	CTC	TGC	AGG	ACA	CCC	TGC	AAC	CTA	1225
	Ala	Glu	Lys	Asp	Ser	Asn	Tyr	Cys	Leu	Cys	Arg	Thr	Pro	Cys	Asn	Leu	
					355					360					365		
70	ACC	CGC	TAC	AAC	AAA	GAG	CTC	TCC	ATG	GTG	AAG	ATC	CCC	AGC	AAG	ACA	1273
	Thr	Arg	Tyr	Asn	Lys	Glu	Leu	Ser	Met	Val	Lys	Ile	Pro	Ser	Lys	Thr	
				370					375					380			

23

INFORMATION CONCERNANT LA SEQ ID NO:4 :

i) CARACTÉRISTIQUE DE LA SEQUENCE :

A) LONGUEUR : 3647 paires de base

5 B) TYPE : acide nucléique

C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

10 vi) ORIGINE : rat

ix) CARACTÉRISTIQUE

A) NOM/CLE : ASIC1B

15 B) LOCALISATION : 109 .. 1785

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:4 :

CTGCCACAGA GGCTCTGGTG AGGAAGGACA GACAGCTGGA CCGGCGCAGA CCTAGCCGAA 60

20 GTCCAACCTC CGTCCCTTCT GGTGGCTTCT TCCTGTCTCC TGAACAAG ATG CCC ATC 117
 Met Pro Ile
 1 3

25 CAG ATC TTT TGT TCT GTG TCA TTC TCC TCT GGA GAG GAG GCC CCG GGA 165
 Gln Ile Phe Cys Ser Val Ser Phe Ser Ser Gly Glu Glu Ala Pro Gly
 5 10 15

30 TCC ATG GCA GAT ATC TGG GGT CCC CAC CAC CAC CGG CAG CAG CAG GAC 213
 Ser Met Ala Asp Ile Trp Gly Pro His His His Arg Gln Gln Gln Asp
 20 25 30 35

35 AGC TCA GAA TCG GAA GAA GAG GAA GAG AAG GAA ATG GAG GCA GGG TCG 261
 Ser Ser Glu Ser Glu Glu Glu Glu Glu Lys Glu Met Glu Ala Gly Ser
 40 45 50

40 GAG TTG GAT GAG GGT GAT GAC TCA CCT AGG GAC TTG GTG GCC TTC GCC 309
 Glu Leu Asp Glu Gly Asp Asp Ser Pro Arg Asp Leu Val Ala Phe Ala
 55 60 65

45 AAC AGC TGT ACC TTC CAT GGT GCC AGC CAT GTG TTT GTG GAA GGG GGC 357
 Asn Ser Cys Thr Phe His Gly Ala Ser His Val Phe Val Glu Gly Gly
 70 75 80

50 CCA GGG CCA AGG CAG GCC TTA TGG GCA GTG GCC TTT GTC ATA GCA CTG 405
 Pro Gly Pro Arg Gln Ala Leu Trp Ala Val Ala Phe Val Ile Ala Leu
 85 90 95

55 GGT GCC TTC CTG TGC CAG GTA GGG GAC CGC GTT GCT TAT TAC CTC AGC 453
 Gly Ala Phe Leu Cys Gln Val Gly Asp Arg Val Ala Tyr Tyr Leu Ser
 100 105 110 115

55 TAC CCA CAC GTG ACT TTG CTA GAC GAA GTG GCC ACC ACG GAG CTG GTC 501
 Tyr Pro His Val Thr Leu Leu Asp Glu Val Ala Thr Thr Glu Leu Val
 120 125 130

	TTC	CCA	GCT	GTC	ACC	TTC	TGC	AAC	ACC	AAT	GCC	GTG	CGG	TTG	TCC	CAG	549
	Phe	Pro	Ala	Val	Thr	Phe	Cys	Asn	Thr	Asn	Ala	Val	Arg	Leu	Ser	Gln	
				135					140					145			
5	CTC	AGC	TAC	CCT	GAC	TTG	CTC	TAC	CTG	GCC	CCC	ATG	CTA	GGA	CTG	GAT	597
	Leu	Ser	Tyr	Pro	Asp	Leu	Leu	Tyr	Leu	Ala	Pro	Met	Leu	Gly	Leu	Asp	
			150					155					160				
10	GAG	AGT	GAT	GAC	CCC	GGG	GTG	CCC	CTT	GCT	CCT	CCT	GGC	CCA	GAG	GCT	645
	Glu	Ser	Asp	Asp	Pro	Gly	Val	Pro	Leu	Ala	Pro	Pro	Gly	Pro	Glu	Ala	
		165					170					175					
15	TTC	TCC	GGG	GAG	CCT	TTT	AAC	CTC	CAT	CGT	TTC	TAT	AAT	CGC	TCT	TGC	693
	Phe	Ser	Gly	Glu	Pro	Phe	Asn	Leu	His	Arg	Phe	Tyr	Asn	Arg	Ser	Cys	
	180					185					190					195	
20	CAC	CGG	CTG	GAG	GAC	ATG	CTG	CTC	TAT	TGT	TCC	TAC	TGT	GGG	GGC	CCC	741
	His	Arg	Leu	Glu	Asp	Met	Leu	Leu	Tyr	Cys	Ser	Tyr	Cys	Gly	Gly	Pro	
					200					205					210		
25	TGT	GGT	CCC	CAC	AAC	TTC	TCA	GTG	GTC	TTC	ACT	CGG	TAT	GGG	AAG	TGT	789
	Cys	Gly	Pro	His	Asn	Phe	Ser	Val	Val	Phe	Thr	Arg	Tyr	Gly	Lys	Cys	
				215					220					225			
30	TAC	ACA	TTC	AAC	TCG	GGC	CAA	GAT	GGG	CGG	CCA	CGG	CTG	AAG	ACC	ATG	837
	Tyr	Thr	Phe	Asn	Ser	Gly	Gln	Asp	Gly	Arg	Pro	Arg	Leu	Lys	Thr	Met	
			230					235					240				
35	AAA	GGT	GGG	ACT	GGC	AAT	GGC	CTG	GAG	ATC	ATG	CTG	GAC	ATT	CAG	CAA	885
	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	Glu	Ile	Met	Leu	Asp	Ile	Gln	Gln	
		245					250					255					
40	GAT	GAA	TAT	TTG	CCT	GTG	TGG	GGA	GAG	ACC	GAC	GAG	ACA	TCC	TTC	GAA	933
	Asp	Glu	Tyr	Leu	Pro	Val	Trp	Gly	Glu	Thr	Asp	Glu	Thr	Ser	Phe	Glu	
	260					265					270					275	
45	GCA	GGC	ATC	AAA	GTG	CAG	ATC	CAC	AGT	CAG	GAT	GAA	CCC	CCT	TTC	ATC	981
	Ala	Gly	Ile	Lys	Val	Gln	Ile	His	Ser	Gln	Asp	Glu	Pro	Pro	Phe	Ile	
					280					285					290		
50	GAC	CAG	CTG	GGC	TTT	GGT	GTG	GCT	CCA	GGT	TTC	CAG	ACG	TTT	GTG	TCT	1029
	Asp	Gln	Leu	Gly	Phe	Gly	Val	Ala	Pro	Gly	Phe	Gln	Thr	Phe	Val	Ser	
				295					300					305			
55	TGC	CAG	GAG	CAG	AGG	CTC	ATC	TAC	CTG	CCC	TCA	CCC	TGG	GGC	ACC	TGC	1077
	Cys	Gln	Glu	Gln	Arg	Leu	Ile	Tyr	Leu	Pro	Ser	Pro	Trp	Gly	Thr	Cys	
			310					315					320				
60	AAT	GCT	GTT	ACC	ATG	GAC	TCG	GAT	TTC	TTC	GAC	TCC	TAC	AGC	ATC	ACT	1125
	Asn	Ala	Val	Thr	Met	Asp	Ser	Asp	Phe	Phe	Asp	Ser	Tyr	Ser	Ile	Thr	
		325					330					335					
65	GCC	TGC	CGG	ATT	GAT	TGC	GAG	ACG	CGT	TAC	CTG	GTG	GAG	AAC	TGC	AAC	1173
	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	Arg	Tyr	Leu	Val	Glu	Asn	Cys	Asn	
		340				345					350					355	

	TGC	CGT	ATG	GTG	CAC	ATG	CCA	GGG	GAC	GCC	CCA	TAC	TGC	ACT	CCA	GAG	1221
	Cys	Arg	Met	Val	His	Met	Pro	Gly	Asp	Ala	Pro	Tyr	Cys	Thr	Pro	Glu	
					360					365					370		
5	CAG	TAC	AAG	GAG	TGT	GCA	GAT	CCT	GCC	CTG	GAC	TTC	CTA	GTG	GAG	AAA	1269
	Gln	Tyr	Lys	Glu	Cys	Ala	Asp	Pro	Ala	Leu	Asp	Phe	Leu	Val	Glu	Lys	
				375					380					385			
10	GAC	CAG	GAA	TAC	TGC	GTG	TGT	GAG	ATG	CCT	TGC	AAC	CTG	ACC	CGC	TAC	1317
	Asp	Gln	Glu	Tyr	Cys	Val	Cys	Glu	Met	Pro	Cys	Asn	Leu	Thr	Arg	Tyr	
			390					395					400				
15	GGC	AAG	GAG	CTG	TCC	ATG	GTC	AAG	ATC	CCA	AGC	AAA	GCC	TCC	GCC	AAG	1365
	Gly	Lys	Glu	Leu	Ser	Met	Val	Lys	Ile	Pro	Ser	Lys	Ala	Ser	Ala	Lys	
		405					410					415					
20	TAC	CTG	GCC	AAG	AAG	TTC	AAC	AAA	TCG	GAG	CAG	TAC	ATA	GGG	GAG	AAC	1413
	Tyr	Leu	Ala	Lys	Lys	Phe	Asn	Lys	Ser	Glu	Gln	Tyr	Ile	Gly	Glu	Asn	
	420					425						430				435	
25	ATT	CTG	GTG	CTG	GAC	ATT	TTC	TTT	GAA	GTC	CTC	AAC	TAT	GAG	ACC	ATC	1461
	Ile	Leu	Val	Leu	Asp	Ile	Phe	Phe	Glu	Val	Leu	Asn	Tyr	Glu	Thr	Ile	
					440				445						450		
30	GAG	CAG	AAA	AAG	GCC	TAT	GAG	ATC	GCA	GGG	CTG	TTG	GGT	GAC	ATC	GGG	1509
	Glu	Gln	Lys	Lys	Ala	Tyr	Glu	Ile	Ala	Gly	Leu	Leu	Gly	Asp	Ile	Gly	
				455					460					465			
35	GGC	CAG	ATG	GGG	TTG	TTC	ATC	GGT	GCC	AGC	ATC	CTC	ACC	GTG	CTG	GAA	1557
	Gly	Gln	Met	Gly	Leu	Phe	Ile	Gly	Ala	Ser	Ile	Leu	Thr	Val	Leu	Glu	
			470					475					480				
40	CTC	TTT	GAC	TAT	GCC	TAC	GAG	GTC	ATT	AAG	CAC	AGG	CTG	TGC	AGA	CGT	1605
	Leu	Phe	Asp	Tyr	Ala	Tyr	Glu	Val	Ile	Lys	His	Arg	Leu	Cys	Arg	Arg	
		485					490					495					
45	GGA	AAG	TGC	CAG	AAG	GAG	GCT	AAG	AGG	AGC	AGC	GCA	GAC	AAG	GGC	GTG	1653
	Gly	Lys	Cys	Gln	Lys	Glu	Ala	Lys	Arg	Ser	Ser	Ala	Asp	Lys	Gly	Val	
	500					505					510					515	
50	GCG	CTC	AGC	CTG	GAT	GAC	GTC	AAA	AGA	CAC	AAT	CCC	TGC	GAG	AGC	CTC	1701
	Ala	Leu	Ser	Leu	Asp	Asp	Val	Lys	Arg	His	Asn	Pro	Cys	Glu	Ser	Leu	
					520					525					530		
55	CGA	GGA	CAT	CCT	GCC	GGG	ATG	ACG	TAC	GCT	GCC	AAC	ATC	CTA	CCT	CAC	1749
	Arg	Gly	His	Pro	Ala	Gly	Met	Thr	Tyr	Ala	Ala	Asn	Ile	Leu	Pro	His	
				535					540					545			
60	CAT	CCC	GCT	CGA	GGC	ACG	TTT	GAG	GAC	TTT	ACC	TGC	TAA	GCCCTCGCAG			1798
	His	Pro	Ala	Arg	Gly	Thr	Phe	Glu	Asp	Phe	Thr	Cys	*				
			550					55				559					
	GCCGCTGTAC CAAAGGCCTA GGTGGGGAGG GCTGGGGGAG CAAGGGGCCC CCAACTGCCC																1858
65	CCAGCTACCC TGTGGACTTA ACTGCATTCC TGGTCAGTGG TTCCCTCTTG TCTGTGGTGA																1918
	GAAAGGAGTC TTGACCATAG AGTCCTCTCC CAGCCTCTAT CCCATCTTTT TATTTTAATT																1978
	TAATCACATT TGCTCTGTAA TATTGCTTGA GGCTGGGGAT CGTGATTTC CCCCAGTTCT																2038

	TTTATTGTTG	AGAATAGTTT	TCTCTATTCT	GGGTTTTCTG	TTATTTCAAA	TGAATCTGCA	2098
	AATTGCTCTT	CCCATCTCTA	TGAAGAATTG	CGTTGGAATT	TTGATGGGGA	TTGTATTGAA	2158
5	TCTGTAGATT	GCCTTTGGTA	AGATGGCCAT	TTTTACTATG	TTAATCCTGC	CAATTCATGA	2218
	GCAAGGGAGA	TCTTTCTATC	TCTGAAATCT	ACTTCAGTTT	CTTTCTTCAG	AGACTTGAAG	2278
10	TTCTTGTCAT	AAAAATCTTT	TTGGTTAGAG	CCACACCAAG	GTATTTTATA	TTGTTTGTGA	2338
	CTATTGTGAA	TGGTGTCATT	TCCCTAATTT	CCTTCTCAGC	CTACTTATCC	TTTGAGTAGA	2398
	GGAAGGCTTC	TGATTTGTTT	GGGTTAATTT	TATACCCAGC	TGCTTTGCTA	AAGTTCTTTA	2458
15	TCAGGTTTAG	GTGTTCTCTG	GTGGAACCTT	TGGGGTCACG	TAAGAATACT	ATTATATCAT	2518
	CTGCAAATAG	TGATATTTC	CTTCTTCCTT	TCCAATTTCT	ATCCCTCTGG	GGACTTTTTG	2578
20	TTGTCTAATT	GCTCTGGCTA	GGACTTCAAA	TTCTATATTG	AATAGATAGG	GAGAGAGTGG	2638
	GCAGCCTTGT	CTAGTTCCTG	GTTTTCGTGG	GATCGCTTCA	AATTTCTCTC	CATTTAGTTT	2698
	GATATTGGCT	ACTGGTTTGC	TGTATATGGC	TTTTACTGTA	CTTAGGTATG	GGCCTTGAAT	2758
25	TCCTGATATT	TCCAAGACTT	TTAACATGAA	GGGGTTTTGA	AATTTGCCAA	ATGCTTTCTC	2818
	AGCATCTAAT	GAGATGATCA	TGTGCCCTCC	CCCCACCTTG	AGTTTGTTTA	TATAGTGGGT	2878
30	TACATGAAAG	GATCATTTCT	AATAGTCCAC	AAGTCTGCCA	AATCTTGCTG	ATTGTGACTC	2938
	ATTTCCATAG	CAGGCTCTAT	AACTTCTCTA	ACAGATTGCA	TTAAACTCTG	CTTGGGGAAG	2998
	GCATTACCTC	TTGGTTGAAG	CAATGTTGTA	GTTTCTATGC	CTGCTGAGTA	AATAGCCTCA	3058
35	AGTCCAAGTA	CTTGCCCGA	CTAATGATCA	AACGTATCCA	GGAGTTCCAT	ACCAGAGATG	3118
	TACTCTTCTC	TCCTTTGAAG	TACATTGCTG	GAAGAGTAAT	TGTGTTTGCT	AGAGATACTC	3178
40	CTTCGAACTG	CAAAAGAAAT	CTCTTGGCTA	AGCATATAAT	CAAGCCTCAG	GTTTTCTTTT	3238
	TATTAAATAG	CTGCTTGTA	GAAAGTGGAC	ACTAAGCATA	TACCTCAAAG	GGAGACAGAA	3298
	TGACTCTGTG	CCTTCACTGA	TGGAAGTCTG	GGTTACAAAT	TACATCAGAA	GAACCTATCA	3358
45	TAGTGAAACA	TCTCATTTCC	CTGGTATAAT	CCCTTCTAGA	AATACACTTG	TGACTCTGAA	3418
	ATGTTATAAT	CGTGACAACT	AGGCTGTTAC	AGATACACCA	AGTTAAATTT	GATAGAGAAA	3478
50	CCAGGCTTGG	AGCCTCATGT	CCATAGGGCA	AGAGGAAGAT	GCTGAGTGTT	TAAGGTTGGT	3538
	TTGAGCGAAG	AACAATACCT	TGTGTCACAA	AAATGAAAGG	AAAAAAGAAA	AAAGGAAAGA	3598
	AGGAAAGAAA	GAGAGAGAAA	GAAAAAGAAA	GAAAGAAAAA	AAAAAAGAAA		3647

INFORMATION CONCERNANT LA SEQ ID NO:5 :

i) CARACTERISTIQUE DE LA SEQUENCE :
 A) LONGUEUR 1602 paires de base
 5 B) TYPE : acide nucléique
 C) NOMBRE DE BRINS : double
 D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN
 10 vi) ORIGINE : rat

ix) CARACTERISTIQUE
 A) NOM/CLE : DRASIC
 B) LOCALISATION : 1 .. 1602
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xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:5 :

20	ATG AAA CCT CGC TCC GGA CTG GAG GAG GCC CAG CGG CGA CAG GCC TCA	48
	Met Lys Pro Arg Ser Gly Leu Glu Glu Ala Gln Arg Arg Gln Ala Ser	
	1 5 10 15	
25	GAC ATC CGG GTG TTT GCC AGC AGC TGC ACA ATG CAT GGT CTG GGC CAC	96
	Asp Ile Arg Val Phe Ala Ser Ser Cys Thr Met His Gly Leu Gly His	
	20 25 30	
30	ATC TTT GGC CCT GGA GGC CTG ACC CTG CGC CGA GGG CTG TGG GCC ACA	144
	Ile Phe Gly Pro Gly Gly Leu Thr Leu Arg Arg Gly Leu Trp Ala Thr	
	35 40 45	
35	GCT GTG CTC CTG TCG CTG GCG GCC TTC CTC TAC CAG GTG GCT GAG CGG	192
	Ala Val Leu Leu Ser Leu Ala Ala Phe Leu Tyr Gln Val Ala Glu Arg	
	50 55 60	
40	GTT CGC TAC TAT GGG GAG TTC CAC CAT AAG ACC ACC CTG GAT GAG CGT	240
	Val Arg Tyr Tyr Gly Glu Phe His His Lys Thr Thr Leu Asp Glu Arg	
	65 70 75 80	
45	GAG AGC CAC CAG CTC ACC TTC CCA GCT GTG ACT CTG TGT AAT ATC AAC	288
	Glu Ser His Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Ile Asn	
	85 90 95	
50	CCA CTG CGC CGC TCA CGC CTC ACA CCC AAT GAC TTG CAC TGG GCT GGA	336
	Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly	
	100 105 110	
55	ACA GCG CTG CTG GGC CTG GAC CCT GCT GAA CAT GCT GCC TAC CTT CGT	384
	Thr Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Tyr Leu Arg	
	115 120 125	
60	GCA CTG GGC CAG CCC CCC GCA CCA CCT GGC TTC ATG CCC AGT CCG ACC	432
	Ala Leu Gly Gln Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr	
	130 135 140	
65	TTT GAC ATG GCA CAA CTC TAC GCC AGA GCC GGC CAC TCC CTT GAG GAC	480
	Phe Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Glu Asp	
	145 150 155 160	

	ATG TTG TTG GAT TGC CGA TAC CGT GGC CAG CCC TGT GGG CCT GAG AAC	528
	Met Leu Leu Asp Cys Arg Tyr Arg Gly Gln Pro Cys Gly Pro Glu Asn	
	165 170 175	
5	TTC ACA GTG ATC TTT ACT CGA ATG GGG CAA TGC TAC ACC TTC AAC TCT	576
	Phe Thr Val Ile Phe Thr Arg Met Gly Gln Cys Tyr Thr Phe Asn Ser	
	180 185 190	
10	GGT GCC CAC GGT GCA GAG CTG CTC ACC ACT CCA AAG GGT GGT GCT GGC	624
	Gly Ala His Gly Ala Glu Leu Leu Thr Thr Pro Lys Gly Gly Ala Gly	
	195 200 205	
15	AAC GGA CTG GAG ATT ATG CTA GAT GTA CAG CAA GAG GAG TAT CTG CCC	672
	Asn Gly Leu Glu Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro	
	210 215 220	
20	ATC TGG AAG GAC ATG GAA GAG ACC CCG TTT GAG GTG GGG ATC CGA GTG	720
	Ile Trp Lys Asp Met Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val	
	225 230 235 240	
25	CAG ATT CAC AGC CAG GAT GAG CCC CCT GCC ATT GAC CAG CTG GGC TTC	768
	Gln Ile His Ser Gln Asp Glu Pro Pro Ala Ile Asp Gln Leu Gly Phe	
	245 250 255	
30	GGG GCA GCC CCA GGC CAT CAG ACT TTT GTG TCC TGT CAG CAG CAG CAA	816
	Gly Ala Ala Pro Gly His Gln Thr Phe Val Ser Cys Gln Gln Gln Gln	
	260 265 270	
35	CTG AGT TTC CTG CCA CCA CCC TGG GGT GAC TGC AAT ACC GCA TCT TTG	864
	Leu Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Asn Thr Ala Ser Leu	
	275 280 285	
40	GAT CCC GAC GAC TTT GAT CCA GAG CCC TCT GAT CCC TTG GGT TCC CCC	912
	Asp Pro Asp Asp Phe Asp Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro	
	290 295 300	
45	AGA CCC AGA CCC AGC CCT CCT TAT AGT TTA ATA GGT TGT CGC CTG GCC	960
	Arg Pro Arg Pro Ser Pro Pro Tyr Ser Leu Ile Gly Cys Arg Leu Ala	
	305 310 315 320	
50	TGT GAG TCT CGC TAT GTG GCT CGG AAG TGT GGC TGT CGA ATG ATG CAT	1008
	Cys Glu Ser Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Met His	
	325 330 335	
55	ATG CCT GGA AAC TCC CCA GTG TGC AGC CCC CAG CAG TAC AAG GAC TGC	1056
	Met Pro Gly Asn Ser Pro Val Cys Ser Pro Gln Gln Tyr Lys Asp Cys	
	340 345 350	
60	GCC AGC CCA GCT CTG GAC GCT ATG CTG CGA AAG GAC ACG TGT GTC TGC	1104
	Ala Ser Pro Ala Leu Asp Ala Met Leu Arg Lys Asp Thr Cys Val Cys	
	355 360 365	
65	CCC AAC CCG TGC GCT ACT ACA CGC TAT GCC AAG GAG CTC TCC ATG GTG	1152
	Pro Asn Pro Cys Ala Thr Thr Arg Tyr Ala Lys Glu Leu Ser Met Val	
	370 375 380	
70	CGG ATT CCC AGC CGC GCG TCA GCT CGC TAC CTG GCC CGG AAA TAC AAC	1200
	Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn	
	385 390 395 400	

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INFORMATION CONCERNANT LA SEQ ID NO:6 :

i) CARACTERISTIQUE DE LA SEQUENCE :

A) LONGUEUR 1948 paires de base

B) TYPE : acide nucléique

C) NOMBRE DE BRINS : double

D) CONFIGURATION : linéaire

ii) TYPE DE MOLECULE : ADN

vi) ORIGINE : rat

ix) CARACTERISTIQUE

A) NOM/CLE : MDEG2

B) LOCALISATION : 16 .. 1707

xi) DESCRIPTION DE LA SEQUENCE : SEQ ID NO:6 :

CCTCGGGCTG AATGA ATG AGC CGG AGC GGC GGA GCC CGG CTG CCC GCG ACC	51
Met Ser Arg Ser Gly Gly Ala Arg Leu Pro Ala Thr	
1 5 10	
GCG CTC AGC GGC CCG GGA CGC TTC CGT ATG GCC CGC GAG CAG CCG GCG	99
Ala Leu Ser Gly Pro Gly Arg Phe Arg Met Ala Arg Glu Gln Pro Ala	
15 20 25	
CCC GTG GCG GTG GCG GCA GCT AGG CAG CCC GGA GGA GAC CGG AGC GGC	147
Pro Val Ala Val Ala Ala Ala Arg Gln Pro Gly Gly Asp Arg Ser Gly	
30 35 40	
GAT CCG GCG CTG CAG GGG CCA GGG GTC GCC CGC AGG GGG CGG CCG TCC	195
Asp Pro Ala Leu Gln Gly Pro Gly Val Ala Arg Arg Gly Arg Pro Ser	
45 50 55 60	
CTG AGT CGC ACT AAA TTG CAC GGG CTG CGG CAC ATG TGC GCG GGG CGC	243
Leu Ser Arg Thr Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg	
65 70 75	
ACG GCG GCG GGA GGC TCT TTC CAG CGA CGG GCG CTG TGG GTG CTG GCC	291
Thr Ala Ala Gly Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala	
80 85 90	
TTC TGC ACG TCC CTC GGC TTG CTG CTG TCC TGG TCC TCG AAC CGC CTG	339
Phe Cys Thr Ser Leu Gly Leu Leu Leu Ser Trp Ser Ser Asn Arg Leu	
95 100 105	
CTC TAC TGG CTC AGC TTC CCG TCA CAC ACA CGA GTG CAC CGT GAG TGG	387
Leu Tyr Trp Leu Ser Phe Pro Ser His Thr Arg Val His Arg Glu Trp	
110 115 120	
AGC CGC CAG CTG CCG TTC CCC GCC GTC ACC GTG TGC AAC AAC AAC CCC	435
Ser Arg Gln Leu Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro	
125 130 135 140	
CTG CGC TTC CCG CGC CTC TCC AAG GGG GAC CTC TAC TAC GCG GGC CAC	483
Leu Arg Phe Pro Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His	
145 150 155	

	TGG	CTA	GGG	CTG	CTG	CTT	CCC	AAC	CGC	ACC	GCG	CGC	CCG	CTG	GTC	AGC	531
	Trp	Leu	Gly	Leu	Leu	Leu	Pro	Asn	Arg	Thr	Ala	Arg	Pro	Leu	Val	Ser	
			160					165					170				
5	GAG	CTG	CTG	CGG	GGC	GAC	GAG	CCG	CGC	CGC	CAG	TGG	TTC	CGC	AAA	CTG	579
	Glu	Leu	Leu	Arg	Gly	Asp	Glu	Pro	Arg	Arg	Gln	Trp	Phe	Arg	Lys	Leu	
			175					180					185				
10	GCC	GAC	TTC	CGC	CTC	TTC	CTG	CCG	CCG	CGC	CAC	TTC	GAG	GGC	ATC	AGC	627
	Ala	Asp	Phe	Arg	Leu	Phe	Leu	Pro	Pro	Arg	His	Phe	Glu	Gly	Ile	Ser	
		190					195					200					
15	GCT	GCC	TTC	ATG	GAC	CGT	TTG	GGC	CAC	CAG	CTG	GAG	GAT	ATG	CTG	CTC	675
	Ala	Ala	Phe	Met	Asp	Arg	Leu	Gly	His	Gln	Leu	Glu	Asp	Met	Leu	Leu	
	205					210					215					220	
20	TCC	TGC	AAG	TAC	CGG	GGC	GAG	CTC	TGT	GGC	CCG	CAC	AAC	TTC	TCC	TCA	723
	Ser	Cys	Lys	Tyr	Arg	Gly	Glu	Leu	Cys	Gly	Pro	His	Asn	Phe	Ser	Ser	
				225						230					235		
25	GTG	TTT	ACA	AAA	TAC	GGG	AAG	TGT	TAC	ATG	TTT	AAC	TCA	GGC	GAG	GAT	771
	Val	Phe	Thr	Lys	Tyr	Gly	Lys	Cys	Tyr	Met	Phe	Asn	Ser	Gly	Glu	Asp	
				240					245					250			
30	GGC	AAG	CCG	CTG	CTC	ACC	ACG	GTC	AAG	GGG	GGG	ACG	GGC	AAC	GGG	CTG	819
	Gly	Lys	Pro	Leu	Leu	Thr	Thr	Val	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	
			255					260					265				
35	GAG	ATC	ATG	CTG	GAC	ATT	CAG	CAA	GAT	GAG	TAC	CTG	CCC	ATC	TGG	GGA	867
	Glu	Ile	Met	Leu	Asp	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Ile	Trp	Gly	
		270					275					280					
40	GAG	ACA	GAG	GAA	ACA	ACG	TTT	GAA	GCA	GGA	GTG	AAG	GTT	CAG	ATC	CAC	915
	Glu	Thr	Glu	Glu	Thr	Thr	Phe	Glu	Ala	Gly	Val	Lys	Val	Gln	Ile	His	
	285					290					295					300	
45	AGT	CAG	TCT	GAG	CCG	CCT	TTC	ATC	CAA	GAG	CTG	GGC	TTT	GGG	GTG	GCT	963
	Ser	Gln	Ser	Glu	Pro	Pro	Phe	Ile	Gln	Glu	Leu	Gly	Phe	Gly	Val	Ala	
					305					310					315		
50	CCG	GGG	TTC	CAG	ACC	TTC	GTG	GCC	ACA	CAA	GAG	CAG	AGG	CTC	ACA	TAT	1011
	Pro	Gly	Phe	Gln	Thr	Phe	Val	Ala	Thr	Gln	Glu	Gln	Arg	Leu	Thr	Tyr	
				320					325					330			
55	CTG	CCC	CCA	CCA	TGG	GGG	GAG	TGC	CGG	TCC	TCA	GAG	ATG	GGA	CTC	GAC	1059
	Leu	Pro	Pro	Pro	Trp	Gly	Glu	Cys	Arg	Ser	Ser	Glu	Met	Gly	Leu	Asp	
			335					340					345				
60	TTC	TTT	CCT	GTT	TAC	AGC	ATC	ACA	GCC	TGT	CGG	ATT	GAC	TGT	GAG	ACC	1107
	Phe	Phe	Pro	Val	Tyr	Ser	Ile	Thr	Ala	Cys	Arg	Ile	Asp	Cys	Glu	Thr	
		350					355					360					
65	CGC	TAC	ATC	GTG	GAG	AAC	TGT	AAC	TGC	CGC	ATG	GTC	CAC	ATG	CCA	GGG	1155
	Arg	Tyr	Ile	Val	Glu	Asn	Cys	Asn	Cys	Arg	Met	Val	His	Met	Pro	Gly	
	365					370					375					380	

	GAC Asp	GCC Ala	CCT Pro	TTC Phe	TGC Cys 385	ACC Thr	CCT Pro	GAG Glu	CAG Gln	CAC His 390	AAG Lys	GAG Glu	TGT Cys	GCA Ala	GAG Glu 395	CCT Pro	1203
5	GCC Ala	CTC Leu	GGT Gly	CTA Leu 400	CTG Leu	GCA Ala	GAA Glu	AAG Lys	GAC Asp 405	AGC Ser	AAT Asn	TAC Tyr	TGT Cys	CTC Leu 410	TGC Cys	AGG Arg	1251
10	ACA Thr	CCC Pro	TGC Cys 415	AAC Asn	CTG Leu	ACA Thr	CGC Arg	TAC Tyr 420	AAC Asn	AAA Lys	GAG Glu	CTC Leu 425	TCC Ser	ATG Met	GTG Val	AAG Lys	1299
15	ATC Ile 430	CCC Pro	AGC Ser	AAG Lys	ACG Thr	TCA Ser	GCC Ala 435	AAG Lys	TAC Tyr	TTA Leu	GAG Glu	AAG Lys 440	AAA Lys	TTT Phe	AAC Asn	AAA Lys	1347
20	TCG Ser 445	GAA Glu	AAA Lys	TAT Tyr	ATC Ile	TCA Ser 450	GAG Glu	AAC Asn	ATT Ile	CTT Leu 455	GTT Val	CTG Leu	GAC Asp	ATA Ile	TTT Phe	TTT Phe 460	1395
25	GAG Glu	GCG Ala	CTC Leu	AAT Asn 465	TAC Tyr	GAA Glu	ACA Thr	ATT Ile	GAA Glu 470	CAG Gln	AAG Lys	AAG Lys	GCG Ala	TAT Tyr	GAA Glu 475	GTT Val	1443
30	GCT Ala	GCC Ala	TTA Leu	CTT Leu 480	GGT Gly	GAC Asp	ATC Ile	GGT Gly 485	CAG Gln	ATG Met	GGA Gly	CTG Leu 490	TTC Phe	ATT Ile	GGT Gly	1491	
35	GCT Ala	AGT Ser	CTC Leu 495	CTC Leu	ACA Thr	ATA Ile	CTA Leu	GAG Glu 500	CTC Leu	TTT Phe	GAT Asp	TAT Tyr 505	ATT Ile	TAT Tyr	GAG Glu	CTG Leu	1539
40	ATC Ile 510	AAA Lys	GAG Glu	AAG Lys	CTA Leu	TTA Leu	GAC Asp 515	CTG Leu	CTT Leu	GGC Gly	AAA Lys	GAA Glu 520	GAA Glu	GAG Glu	GAA Glu	GGG Gly	1587
45	AGC Ser 525	CAC His	GAT Asp	GAG Glu	AAC Asn	ATG Met 530	AGC Ser	ACC Thr	TGT Cys	GAC Asp	ACA Thr 535	ATG Met	CCA Pro	AAC Asn	CAC His	TCT Ser 540	1635
50	GAA Glu	ACC Thr	ATC Ile	AGC Ser 545	CAC His	ACT Thr	GTG Val	AAC Asn	GTG Val 550	CCC Pro	CTG Leu	CAG Gln	ACA Thr	GCT Ala	TTG Leu 555	GGC Gly	1683
55	ACC Thr	CTG Leu	GAG Glu	GAG Glu 560	ATT Ile	GCC Ala	TGC Cys 563	TGA *	CACCTCTCAG	GCAACGCAGC	ACCTCCAAAC	1737					
60	AGACCTTAAA	GGCCCAAGAC	CTAGGACAGG	AGACAGCAAG	CGCAGGTGGG	ATCGCCCCTG	1797										
65	ACGACTGAAA	GAAGCAGAGC	CCCCCATATG	CACACATTGC	GAACCTTCTGC	CAAACCTCAC	1857										
70	CTGGCCACAT	CTGACATGAA	CCGTCCCGGG	CCCTGCGTCA	TGTCCCTCGC	AGGACCGATG	1917										
75	AGTCGCACTC	CGGAACGTGC	CAAGAACTAA	C			1948										